

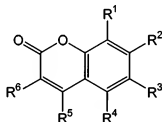
**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

1-83 (canceled)

84 (previously presented): A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R<sup>1</sup>, R<sup>3</sup>, R<sup>4</sup> and R<sup>6</sup> are each H;

R<sup>2</sup> is -NHR<sup>15</sup>; and

R<sup>5</sup> is -R<sup>14</sup>-SS,

wherein:

R<sup>14</sup> is -CH<sub>2</sub>C(O)NH-;

R<sup>15</sup> is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue; and

SS is a solid support.

1                   **85** (previously presented): The material in accordance with claim **84**, wherein  
2     $R^{15}$  is an amine protecting group.

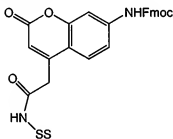
1                   **86** (previously presented): The material in accordance with claim **85**, wherein  
2    said amine protecting group is 9-fluorenylmethoxycarbonyl (Fmoc).

1                   **87** (previously presented): The material in accordance with claim **84**, wherein  
2     $R^{15}$  is  $-C(O)-AA$ , wherein AA is an amino acid residue.

1                   **88** (previously presented): The material in accordance with claim **84**, wherein  
2     $R^{15}$  is  $-C(O)-P$ , wherein P is a peptide sequence.

1                   **89** (previously presented): The material in accordance with claim **84**, wherein  
2    the solid support is a Rink resin.

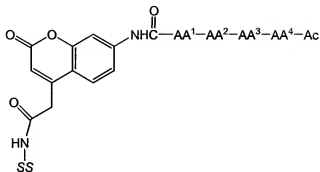
1                   **90** (previously presented): A material having a fluorogenic moiety linked to a  
2    solid support, said material having the structure:



3  
4    wherein:

5                   SS is a solid support, wherein said the support is a Rink resin.

1                   **91** (previously presented): A library of fluorogenic peptides comprising sub-  
2    libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises  
3    tetrapeptides having the structure:



wherein:

SS is a solid support, and

wherein:

for sub-library P1, each AA<sup>1</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>2</sup>-AA<sup>4</sup> is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA<sup>2</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>1</sup>, AA<sup>3</sup> and AA<sup>4</sup> is an isokinetic mixture of 20 amino acids;

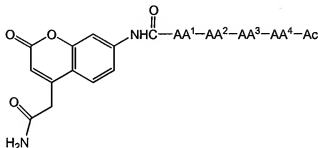
for sub-library P3, each of AA<sup>3</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>1</sup>, AA<sup>2</sup> and AA<sup>4</sup> is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA<sup>4</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>1</sup>, AA<sup>2</sup> and AA<sup>3</sup> is an isokinetic mixture of 20 amino acids.

**92** (previously presented): The library in accordance with claim 91, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

**93** (previously presented): The library in accordance with claim 91, wherein the solid support is a Rink resin.

**94** (previously presented): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the structure:



wherein:

for sub-library P1, each AA<sup>1</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>2</sup>-AA<sup>4</sup> is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA<sup>2</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>1</sup>, AA<sup>3</sup> and AA<sup>4</sup> is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA<sup>3</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>1</sup>, AA<sup>2</sup> and AA<sup>4</sup> is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA<sup>4</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>1</sup>, AA<sup>2</sup> and AA<sup>3</sup> is an isokinetic mixture of 20 amino acids.

**95** (previously presented): The library in accordance with claim **94**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

**96** (previously presented): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim 91 or claim 94 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

97 (previously presented): The method according to claim 96, further comprising

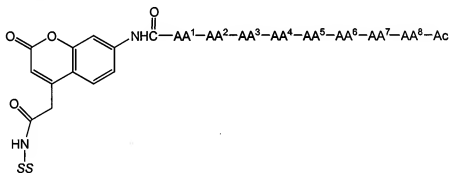
(d) quantifying said fluorescent moiety, thereby quantifying said protease.

98 (previously presented): The method according to claim 97, wherein said

protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

99 (previously presented): A library of fluorogenic peptides comprising sub-

libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

SS is a solid support, and

wherein:

for each sub-library P1, P2, P3 and P4, AA<sup>1</sup>, AA<sup>2</sup>, AA<sup>3</sup> and AA<sup>4</sup> in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA<sup>5</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>6</sup>, AA<sup>7</sup> and AA<sup>8</sup> is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA<sup>6</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>5</sup>, AA<sup>7</sup> and AA<sup>8</sup> is an isokinetic mixture of 20 amino acids;

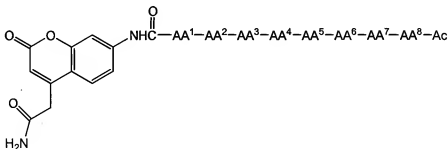
for sub-library P3, each of AA<sup>7</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>5</sup>, AA<sup>6</sup> and AA<sup>8</sup> is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA<sup>8</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>5</sup>, AA<sup>6</sup> and AA<sup>7</sup> is an isokinetic mixture of 20 amino acids.

**100** (previously presented): The library in accordance with claim 99, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

**101** (previously presented): The library in accordance with claim 99, wherein the solid support is a Rink resin.

**102** (previously presented): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

for each sub-library P1, P2, P3 and P4, AA<sup>1</sup>, AA<sup>2</sup>, AA<sup>3</sup> and AA<sup>4</sup> in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA<sup>5</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>6</sup>, AA<sup>7</sup> and AA<sup>8</sup> is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA<sup>6</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>5</sup>, AA<sup>7</sup> and AA<sup>8</sup> is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA<sup>7</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>5</sup>, AA<sup>6</sup> and AA<sup>8</sup> is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA<sup>8</sup> is a different amino acid of the 20 amino acids, and each of AA<sup>5</sup>, AA<sup>6</sup> and AA<sup>7</sup> is an isokinetic mixture of 20 amino acids.

**103** (previously presented): The library in accordance with claim **102**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

**104** (previously presented): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **99** or claim **102** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

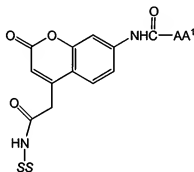
(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

**105** (previously presented): The method according to claim **104**, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

1                   **106** (previously presented): The method according to claim **105**, wherein said  
2 protease is a member selected from the group consisting of aspartic protease, cysteine protease,  
3 metalloprotease and serine protease.

1                   **107** (previously presented): A library of twenty fluorogenic amino acid amides  
2 having the structure:



3  
4 wherein:

5                    $SS$  is a solid support, and

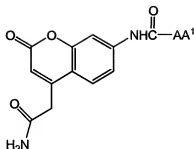
6                   each  $AA^1$  for the twenty fluorogenic amino acid amides is a different amino acid  
7 residue.

1                   **108** (previously presented): The library in accordance with claim **107**, wherein  
2 the amino acid residues are the 20 naturally occurring amino acids excluding cysteine and  
3 including norleucine.

1                   **109** (previously presented): The library in accordance with claim **108**, wherein  
2 the solid support is a Rink resin.

1                   **110** (previously presented): A library of twenty fluorogenic amino acids having  
2 the structure:





wherein:

each AA<sup>1</sup> for the twenty fluorogenic amino acids is a different amino acid residue

**111** (previously presented): The library in accordance with claim 110, wherein the amino acid residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine..

**112** (previously presented): A method of determining an amino acid specificity profile of an enzymatically active protease, said method comprising:

- (a) contacting said protease with a library of amino acids according to claim 108 or claim 110 in such a manner whereby the fluorogenic moiety is released from the amino acid, thereby forming a fluorescent moiety;
- (b) detecting said fluorescent moiety;
- (c) determining the identity of the amino acid, thereby determining said amino acid specificity profile of said protease.

**113** (previously presented): The method according to claim 112, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

**114** (previously presented): The method according to claim 113, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.